AMENDMENTS TO THE CLAIMS

Please cancel Claims 33-37 without prejudice, amend Claims 31, 38 and 40, and add Claims 41-53 as shown in the following listings of the claims:

1-30. (Cancelled).

31. (Currently amended). A method for ~~identifying a predisposition to obesity in a human subject~~ determining whether a subject is at decreased risk of fat deposition comprising ~~which comprises determining the presence or absence of a polymorphic variation associated with obesity~~

(a) detecting the presence or absence of an A allele at position 7328 ~~or a G allele at position 9182 in a nucleotide sequence identical to~~ of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 ~~or 99% identical to SEQ ID NO: 1, or in the corresponding position in the complementary sequence thereof, in a nucleic acid sample from a subject, whereby the presence of the polymorphic variation is indicative of a predisposition to obesity in the subject~~ or the presence of a T allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject, or

(b) detecting the presence or absence of a G allele at position 9182 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or the presence of a C allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject,

wherein (i) the presence of an A allele at position 7328 of the PLA2G1B nucleic acid comprising SEQ ID NO:1, or a T allele at its complementary position of 7328 in the strand complementary to SEQ ID NO:1, or (ii) the presence of a G allele at position 9182 of the PLA2G1B nucleic acid comprising SEQ ID NO:1, or a C allele at its complementary position in the strand complementary to SEQ ID NO:1 indicates that the subject is at decreased risk for fat deposition.

32. (Previously presented) The method of claim 31, which further comprises obtaining the nucleic acid sample from the subject.

33. (Canceled).

34. (Canceled).

35. (Canceled).

36. (Canceled).

37. (Canceled).

38. (Currently amended) The method of claim ~~31~~ 49 wherein ~~detecting the presence or absence of a polymorphic variation~~ the primer extension method comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to the nucleotide sequence and hybridizes to a region of the nucleotide sequence that is adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of the polymorphic variation in the extension products.

39. (Canceled).

40. (Currently amended) The method of claim 31, wherein the ~~obesity~~ fat deposition is central ~~obesity~~ fat deposition.

41. (New) The method of claim 31, wherein the subject is a human.

42. (New) The method of claim 31, wherein the method comprises detecting the presence or absence of an A allele at position 7328 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO:1 or a T allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject.

43. (New) The method of claim 31, wherein the method comprises detecting the presence or absence of a G allele at position 9182 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO:1 or a C allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject.

44. (New) The method of claim 31, wherein the method comprises (a) detecting the presence or absence of an A allele at position 7328 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or a T allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject; and (b) detecting the presence or absence of a G allele at position 9182 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or a C allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject.

45. (New) The method of claim 31, wherein the detecting step comprises amplifying the nucleic acid sample using oligonucleotide primers flanking said allele(s).

46. (New) The method of claim 45, wherein the amplification is performed using oligonucleotides primers of SEQ ID NO:25 and SEQ ID NO:26, or SEQ ID NO:49 and SEQ ID NO:50.

47. (New) The method of claim 45, wherein the amplification is performed using oligonucleotide primers of SEQ ID NO:29 and SEQ ID NO:30, or SEQ ID NO:51 and SEQ ID NO:52.

48. (New) The method of claim 31, wherein said allele(s) are detected by a method selected from the group consisting of: a primer extension method, a ligase sequence determination method, a microarray sequence determination method, a restrict fragment length polymorphism, single strand conformation polymorphism detection, and PCR-based assay and nucleotide sequencing method.

49. (New) The method of claim 48, wherein said allele(s) are detected by a primer extension method.

50. (New) The method of claim 49, wherein the A allele at position 7328 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 is detected by a primer extension method using the oligonucleotide of SEQ ID NO:38 or SEQ ID NO:61.

51. (New) The method of claim 49, wherein the G allele at position 9182 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 is detected by a primer extension method using the oligonucleotide of SEQ ID NO:40 or SEQ ID NO:62.

52. (New) The method of claim 31 further comprising (c) detecting the presence or absence of a T or G allele at position 4050 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or the presence of an A or C allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject; and (d) detecting the presence or absence of a T allele at position 7256 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or an A allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject.

53. (New) A method for determining whether a subject is at increased risk of fat deposition comprising

(a) detecting the presence or absence of an A allele at position 7328 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or a T allele at its complementary position in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject, or

(b) detecting the presence or absence of a G allele at position 9182 of a PLA2G1B nucleic acid comprising the sequence of SEQ ID NO: 1 or a C allele at its complementary positing in a strand complementary to SEQ ID NO:1 in a nucleic acid sample from the subject

wherein (i) the absence of an A allele at position 7328 of the PLA2G1B nucleic acid comprising SEQ ID NO:1, or a T allele at its complementary position of 7328 in the strand complementary to SEQ ID NO:1, or (ii) the absence of a G allele at position 9182 of the PLA2G1B nucleic acid comprising SEQ ID NO:1, or a C allele at its complementary position in the strand complementary to SEQ ID NO:1 indicates that the subject is at increased risk for fat deposition.